

FILE 'HOME' ENTERED AT 09:11:56 ON 12 JUN 2002

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COST IN U.S. DOLLARS

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SESSION

FULL ESTIMATED COST

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FILE 'MEDLINE' ENTERED AT 09:12:08 ON 12 JUN 2002

FILE LAST UPDATED: 11 JUN 2002 (20020611/UP). FILE COVERS 1958 TO DATE.

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THIS FILE CONTAINS CAS REGISTRY NUMBERS FOR EASY AND ACCURATE SUBSTANCE IDENTIFICATION.

=> s prediction (p) (coding sequences) (p) (human genes) (p) clones

38060 PREDICTION

17277 PREDICTIONS

52811 PREDICTION :

(PREDICTION OR PREDICTIONS)

56913 CODING

92 CODINGS

56967 CODING

(CODING OR CODINGS)

170424 SEQUENCES

3770 CODING SEQUENCES

(CODING(W) SEQUENCES)

7718955 HUMAN

101582 HUMANS

7738475 HUMAN

(HUMAN OR HUMANS)

355134 GENES

20 GENESES

355153 GENES

(GENES OR GENESES)

1747 HUMAN GENES

(HUMAN(W) GENES)

53317 CLONES

L1 27 PREDICTION (P) (CODING SEQUENCES) (P) (HUMAN GENES) (P) CLONES

=> s l1 (p) cDNA (p) brain

81145 CDNA

15300 CDNAS

88437 CDNA

(CDNA OR CDNAS)

544478 BRAIN

20866 BRAINS

548623 BRAIN

(BRAIN OR BRAINS)

L2 17 L1 (P) CDNA (P) BRAIN

=> s l2 (p) (large proteines)

386015 LARGE

39 LARGES

386039 LARGE

(LARGE OR LARGES)

1563 PROTEINES

0 LARGE PROTEINES

(LARGE(W) PROTEINES)

L3 0 L2 (P) (LARGE PROTEINES)

=> s l2 (p) (in vitro)

694398 VITRO

49 VITROS

694444 IN VITRO

(VITRO OR VITROS)

L4 15 L2 (P) (IN VITRO)

=> s 14 (p) proteins
901571 PROTEINS
L5 15 L4 (P) PROTEINS

=> s 14 (p) (large proteins)
386015 LARGE
39 LARGES
386039 LARGE
(LARGE OR LARGES)
901571 PROTEINS
377 LARGE PROTEINS
(LARGE(W) PROTEINS)
L6 15 L4 (P) (LARGE PROTEINS)

=> s 16 and py=1998
442735 PY=1998
L7 5 L6 AND PY=1998

=> d 17 1-5 ibib abs

L7 ANSWER 1 OF 5 MEDLINE
ACCESSION NUMBER: 1999156230 MEDLINE
DOCUMENT NUMBER: 99156230 PubMed ID: 10048485
TITLE: ***Prediction*** of the ***coding***
sequences of unidentified ***human***
genes . XII. The complete sequences of 100 new
cDNA ***clones*** from ***brain*** which
code for ***large*** ***proteins*** in
vitro
AUTHOR: Nagase T; Ishikawa K; Suyama M; Kikuno R; Hirose M;
Miyajima N; Tanaka A; Kotani H; Nomura N; Ohara O
CORPORATE SOURCE: Kazusa DNA Research Institute, Kisarazu, Chiba, Japan.
SOURCE: DNA RESEARCH, *** (1998 Dec 31) *** 5 (6) 355-64.
Journal code: 9423827. ISSN: 1340-2838.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB020626; GENBANK-AB020627; GENBANK-AB020628;
GENBANK-AB020629; GENBANK-AB020630; GENBANK-AB020631;
GENBANK-AB020632; GENBANK-AB020633; GENBANK-AB020634;
GENBANK-AB020635; GENBANK-AB020636; GENBANK-AB020637;
GENBANK-AB020638; GENBANK-AB020639; GENBANK-AB020640;
GENBANK-AB020641; GENBANK-AB020642; GENBANK-AB020643;
GENBANK-AB020644; GENBANK-AB020645; GENBANK-AB020646;
GENBANK-AB020647; GENBANK-AB020648; GENBANK-AB020649;
GENBANK-AB020650; GENBANK-AB020651; GENBANK-AB020652;
GENBANK-AB020653; GENBANK-AB020654; GENBANK-AB020655
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990517
Last Updated on STN: 20000303
Entered Medline: 19990506

AB In this paper, we report the sequences of 100 cDNA clones newly determined from a set of size-fractionated human brain cDNA libraries and predict the coding sequences of the corresponding genes, named KIAA0819 to KIAA0918. These cDNA clones were selected on the basis of their coding potentials of large proteins (50 kDa and more) by using in vitro transcription/translation assays. The sequence data showed that the average sizes of the inserts and corresponding open reading frames are 4.4 kb and 2.5 kb (831 amino acid residues), respectively. Homology and motif/domain searches against the public databases indicated that the predicted coding sequences of 83 genes were similar to those of known genes, 59% of which (49 genes) were categorized as coding for proteins functionally related to cell signaling/communication, cell structure/motility and nucleic acid management. The chromosomal locations and the expression profiles of all the genes were also examined. For 54 clones including brain-specific ones, the mRNA levels were further examined among 8 brain regions (amygdala, corpus callosum, cerebellum, caudate nucleus, hippocampus, substantia nigra, subthalamic nucleus, and thalamus), spinal cord, and fetal brain.

L7 ANSWER 2 OF 5 MEDLINE
 ACCESSION NUMBER: 1999087487 MEDLINE
 DOCUMENT NUMBER: 99087487 PubMed ID: 9872452
 TITLE: ***Prediction*** of the ***coding***
 sequences of unidentified ***human***
 genes . XI. The complete sequences of 100 new
 cDNA ***clones*** from ***brain*** which
 code for ***large*** ***proteins*** in
 vitro .
 AUTHOR: Nagase T; Ishikawa K; Suyama M; Kikuno R; Miyajima N;
 Tanaka A; Kotani H; Nomura N; Ohara O
 CORPORATE SOURCE: Kazusa DNA Research Institute, Kisarazu, Chiba, Japan.
 SOURCE: DNA RESEARCH, *** (1998 Oct 30) *** 5 (5) 277-86.
 Journal code: 9423827. ISSN: 1340-2838.
 PUB. COUNTRY: Japan
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB018254; GENBANK-AB018255; GENBANK-AB018256;
 GENBANK-AB018257; GENBANK-AB018258; GENBANK-AB018259;
 GENBANK-AB018260; GENBANK-AB018261; GENBANK-AB018262;
 GENBANK-AB018263; GENBANK-AB018264; GENBANK-AB018265;
 GENBANK-AB018266; GENBANK-AB018267; GENBANK-AB018268;
 GENBANK-AB018269; GENBANK-AB018270; GENBANK-AB018271;
 GENBANK-AB018272; GENBANK-AB018273; GENBANK-AB018274;
 GENBANK-AB018275; GENBANK-AB018276; GENBANK-AB018277;
 GENBANK-AB018278; GENBANK-AB018279; GENBANK-AB018280;
 GENBANK-AB018281; GENBANK-AB018282; GENBANK-AB018283; +
 ENTRY MONTH: 199904
 ENTRY DATE: Entered STN: 19990504
 Last Updated on STN: 19990504
 Entered Medline: 19990419

AB In our series of projects for accumulating sequence information on the
 coding sequences of unidentified human genes, we have newly determined the
 sequences of 100 cDNA clones from a set of size-fractionated human brain
 cDNA libraries, and predicted the coding sequences of the corresponding
 genes, named KIAA0711 to KIAA0810. These cDNA clones were selected
 according to their coding potentials of large proteins (50 kDa and more)
 in vitro. The average sizes of the inserts and corresponding open reading
 frames were 4.3 kb and 2.6 kb (869 amino acid residues), respectively.
 Sequence analyses against the public databases indicated that the
 predicted coding sequences of 78 genes were similar to those of known
 genes, 64% of which (50 genes) were categorized as proteins functionally
 related to cell signaling/communication, cell structure/motility and
 nucleic acid management. As additional information concerning genes
 characterized in this study, the chromosomal locations of the clones were
 determined by using human-rodent hybrid panels and the expression profiles
 among 10 human tissues were examined by reverse transcription-coupled
 polymerase chain reaction which was substantially improved by
 enzyme-linked immunosorbent assay.

L7 ANSWER 3 OF 5 MEDLINE
 ACCESSION NUMBER: 1998403880 MEDLINE
 DOCUMENT NUMBER: 98403880 PubMed ID: 9734811
 TITLE: ***Prediction*** of the ***coding***
 sequences of unidentified ***human***
 genes . X. The complete sequences of 100 new
 cDNA ***clones*** from ***brain*** which
 can code for ***large*** ***proteins*** in
 vitro .
 AUTHOR: Ishikawa K; Nagase T; Suyama M; Miyajima N; Tanaka A;
 Kotani H; Nomura N; Ohara O
 CORPORATE SOURCE: Kazusa DNA Research Institute, Kisarazu, Chiba, Japan.
 SOURCE: DNA RESEARCH, *** (1998 Jun 30) *** 5 (3) 169-76.
 Journal code: 9423827. ISSN: 1340-2838.
 PUB. COUNTRY: Japan
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB014511; GENBANK-AB014512; GENBANK-AB014513;
 GENBANK-AB014514; GENBANK-AB014515; GENBANK-AB014516;
 GENBANK-AB014517; GENBANK-AB014518; GENBANK-AB014519;

GENBANK-AB014521; GENBANK-AB014522;
 GENBANK-AB014523; GENBANK-AB014524; GENBANK-AB014525;
 GENBANK-AB014526; GENBANK-AB014527; GENBANK-AB014528;
 GENBANK-AB014529; GENBANK-AB014530; GENBANK-AB014531;
 GENBANK-AB014532; GENBANK-AB014533; GENBANK-AB014534;
 GENBANK-AB014535; GENBANK-AB014536; GENBANK-AB014537;
 GENBANK-AB014538; GENBANK-AB014539; GENBANK-AB014540; +

ENTRY MONTH:

199812

ENTRY DATE:

Entered STN: 19990115

Last Updated on STN: 19990115

Entered Medline: 19981209

AB As an extension of our cDNA analysis for deducing the coding sequences of unidentified human genes, we have newly determined the sequences of 100 cDNA clones from a set of size-fractionated human brain cDNA libraries, and predicted the coding sequences of the corresponding genes, named KIAA0611 to KIAA0710. In vitro transcription-coupled translation assay was applied as the first screening to select cDNA clones which produce proteins with apparent molecular mass of 50 kDa and over. One hundred unidentified cDNA clones thus selected were then subjected to sequencing of entire inserts. The average size of the inserts and corresponding open reading frames was 4.9 kb and 2.8 kb (922 amino acid residues), respectively. Computer search of the sequences against the public databases indicated that predicted coding sequences of 87 genes were similar to those of known genes, 62% of which (54 genes) were categorized as proteins related to cell signaling/communication, cell structure/motility and nucleic acid management. The expression profiles in 10 human tissues of all the clones characterized in this study were examined by reverse transcription-coupled polymerase chain reaction and the chromosomal locations of the clones were determined by using human-rodent hybrid panels.

L7 ANSWER 4 OF 5

MEDLINE

ACCESSION NUMBER:

1998340016

MEDLINE

DOCUMENT NUMBER:

98340016

PubMed ID: 9675416

TITLE:

Characterization of a new beta-spectrin gene which is predominantly expressed in brain.

AUTHOR:

Ohara O; Ohara R; Yamakawa H; Nakajima D; Nakayama M

CORPORATE SOURCE:

Laboratory of DNA Technology, Kazusa DNA Research Institute, Chiba, Japan.. ohara@kazusa.or.jp

SOURCE:

BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, *** (1998 Jun) ***
 *** 15) *** 57 (2) 181-92.

Journal code: 8908640. ISSN: 0169-328X.

PUB. COUNTRY:

Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

OTHER SOURCE:

GENBANK-AB008551; GENBANK-AB008567

ENTRY MONTH:

199810

ENTRY DATE:

Entered STN: 19981029

Last Updated on STN: 20000303

Entered Medline: 19981020

AB We recently identified a gene which shows high similarity to the beta-spectrin gene but with a different chromosomal location from either of the two known beta-spectrin genes [T. Nagase, K.-I. Ishikawa, D. Nakajima, M. Ohira, N. Seki, N. Miyajima, A. Tanaka, H. Kotani, N. Nomura, O. Ohara, ***Prediction*** of the ***coding*** ***sequences*** of unidentified ***human*** ***genes*** : VII. The complete sequences of 100 new ***cDNA*** ***clones*** from ***brain*** which can code for ***large*** ***proteins*** in ***vitro***, DNA Res. 4 (1997) 141-150]. In order to further characterize this new spectrin gene and its product, we isolated the rat counterpart of this gene and analyzed it in terms of its protein coding sequence, the tissue distribution of its mRNA and the product, and the regional distribution of the mRNA and the product in the ***brain***. The results indicated that this gene was most abundantly transcribed in the ***brain*** and neurons were the predominant cell-type to express this gene. In particular, Purkinje cells were the richest in this gene product, and this new form of beta-spectrin was found more prominently in the dendrites than in the cell bodies. Since the expression pattern and the subcellular localization of this gene product were quite distinct from those of the two beta-spectrin isoforms already characterized, this beta-spectrin gene would play an important role in neuronal membrane skeleton although it has

been overlooked to date.

L7 ANSWER 5 OF 5 MEDLINE
ACCESSION NUMBER: 1998290545 MEDLINE
DOCUMENT NUMBER: 98290545 PubMed ID: 9628581
TITLE: ***Prediction*** of the ***coding***
sequences of unidentified ***human***
genes . IX. The complete sequences of 100 new
cDNA ***clones*** from ***brain*** which
can code for ***large*** ***proteins*** in
vitro .
AUTHOR: Nagase T; Ishikawa K; Miyajima N; Tanaka A; Kotani H;
Nomura N; Ohara O
CORPORATE SOURCE: Kazusa DNA Research Institute, Kisarazu, Chiba, Japan.
SOURCE: DNA RESEARCH, *** (1998 Feb 28) *** 5 (1) 31-9.
Journal code: 9423827. ISSN: 1340-2838.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB011083; GENBANK-AB011084; GENBANK-AB011085;
GENBANK-AB011086; GENBANK-AB011087; GENBANK-AB011088;
GENBANK-AB011089; GENBANK-AB011090; GENBANK-AB011091;
GENBANK-AB011092; GENBANK-AB011093; GENBANK-AB011094;
GENBANK-AB011095; GENBANK-AB011096; GENBANK-AB011097;
GENBANK-AB011098; GENBANK-AB011099; GENBANK-AB011100;
GENBANK-AB011101; GENBANK-AB011102; GENBANK-AB011103;
GENBANK-AB011104; GENBANK-AB011105; GENBANK-AB011106;
GENBANK-AB011107; GENBANK-AB011108; GENBANK-AB011109;
GENBANK-AB011110; GENBANK-AB011111; GENBANK-AB011112
ENTRY MONTH: 199808
ENTRY DATE: Entered STN: 19980903
Last Updated on STN: 20000303
Entered Medline: 19980825

AB As an extension of a series of projects for sequencing human cDNA clones derived from relatively long transcripts, we herein report the entire sequences of 100 newly determined cDNA clones with the potential of coding for large proteins in vitro. The cDNA clones were isolated from size-fractionated human brain cDNA libraries with insert sizes between 4.5 and 8.3 kb. The sequencing of these clones revealed that the average size of the cDNA inserts and of their open reading frames was 5.3 kb and 2.8 kb (930 amino acid residues), respectively. Homology search against public databases indicated that the predicted coding sequences of 86 clones exhibited significant similarities to known genes; 51 of them (59%) were related to those for cell signaling/communication, nucleic acid management, and cell structure/motility. All the clones characterized in this study are accompanied by their expression profiles in 14 human tissues examined by reverse transcription-coupled polymerase chain reaction and the chromosomal mapping data.

=> log y

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
4.04	4.25

FULL ESTIMATED COST

STN INTERNATIONAL LOGOFF AT 09:17:08 ON 12 JUN 2002